AMENDMENTS TO THE CLAIMS

This Listing of Claims will replace all prior versions and listings of claims in this application.

Listing of Claims

Claims 1-44 (Canceled).

Claim 45 (Currently amended). A culture-independent method of determining the abundance of an environmental parameter in an environmental sample, said parameter not including bacteria, comprising the steps of:

    a.   providing a first plurality of environmental samples at least some of which samples contain the environmental parameter;

    b.   isolating a plurality of genomic DNAs from each of the samples provided in step a;

    c.   isolating a plurality of 16S rRNA gene segments from each plurality of genomic DNAs isolated in step b;

    d.   determining the abundance of each of said 16S rRNA gene segments in each plurality of 16S rRNA gene segments isolated in step c;

    e.   determining the abundance of the environmental parameter in each of the samples provided in step a;

    f.   correlating the abundance of each 16S rRNA gene segment determined in step d with the abundance of the environmental parameter determined in step e;

    g.   selecting at least one 16S rRNA gene segment whose abundance correlates to the abundance of said environmental parameter, as determined in step f;

    h.   providing an environmental sample set of at least one environmental sample;

    i.   isolating a plurality of genomic DNAs from each environmental sample of the environmental sample set provided in step h;

j.   determining the abundance of said 16S rRNA gene segment selected in step g in each plurality of genomic DNAs isolated in step i; and

k.   inferring the abundance of the environmental parameter in each environmental sample of the environmental sample set provided in step h based upon the abundance of said 16S rRNA gene determined in step j in each environmental sample of the environmental sample set provided in step h.

Claim 46 (Canceled)

Claim 47 (Previously amended). The method according to claim 45, wherein the correlation in step g is expressed by an r-value of 1.

Claim 48 (Previously amended). The method according to claim 45, wherein the correlation in step g is expressed by an r-value of 0.8 to 0.99.

Claim 49 (Previously amended). The method according to claim 45, wherein the correlation in step g is expressed by an r-value of 0.5 to 0.7.

Claim 50 (Previously amended). The method according to claim 45, wherein the environmental parameter is subsurface oil or natural gas.

Claim 51 (Withdrawn, currently amended). The method according to claim 45, 60 or 65 or claim 46, wherein the environmental parameter of interest is a dynamic change that occurs during an oil and gas deposit's development that affects its hydrocarbon composition, migration, depletion, and hydrogen sulfide production.

Claim 52 (Withdrawn, currently amended). The method according to claim 45, 60 or 65 or claim 46, wherein the environmental parameter of interest is a mineral deposit.

Claim 53 (Withdrawn, currently amended). The method according to claim 45, 60 or 65 or claim 46, wherein the environmental parameter of interest is an indicator of the mineral deposit's composition.

Claim 54 (Withdrawn, currently amended). The method according to claim 45, 60 or 65 or claim 46, wherein the environmental parameter of interest is an agricultural pest.

Claim 55 (Withdrawn, currently amended). The method according to claim 45, 60 or 65 or claim 46, wherein the environmental parameter of interest is an industrial organic chemical.

Claim 56 (Withdrawn, currently amended). The method according to claim 45, 60 or 65 or claim 46, wherein the environmental parameter of interest is water.

Claim 57 (Canceled)

Claim 58 (Previously submitted). The method of claim 45, wherein the determination in step j, of the abundance of said 16S rRNA gene segment, is done using PCR.

Claim 59 (Previously submitted). The method of claim 45, wherein the determination in step j, of the abundance of said 16S rRNA gene segment, is done using a hybridization assay.

Claim 60 (Currently amended). A culture-independent method of identifying an indicator for an environmental parameter, said parameter not including bacteria, said method comprising the steps of:

    a.   providing a plurality of environmental samples at least some of which samples contain the environmental parameter;

    b.   isolating a plurality of genomic DNAs from each of the samples provided in step a;

    c.   isolating a plurality of 16S rRNA gene segments from each plurality of genomic DNAs isolated in step b;

    d.   determining the abundance of each of said 16S rRNA gene segments in each plurality of 16S rRNA gene segments isolated in step c;

    e.   determining the abundance of the environmental parameter in each of the samples provided in step a;

  f. correlating the abundance of each 16S rRNA gene segment determined in step d with the abundance of the environmental parameter determined in step e;

  g. selecting at least one 16S rRNA gene segment whose abundance correlates to the abundance of said environmental parameter, as determined in step f;

  h. designating said 16S rRNA gene segment as the indicator.

Claim 61 (Previously submitted). The method according to claim 60, wherein the correlation in step g is expressed by an r-value of 1.

Claim 62 (Previously submitted). The method according to claim 60, wherein the correlation in step g is expressed by an r-value of 0.8 to 0.99.

Claim 63 (Previously submitted). The method according to claim 60, wherein the correlation in step g is expressed by an r-value of 0.5 to 0.7.

Claim 64 (Previously submitted). The method according to claim 60, wherein the environmental parameter is subsurface oil or natural gas.

Claim 65 (Currently amended). A culture-independent method of determining the abundance of an environmental parameter in an environmental sample, said parameter not including bacteria, comprising the steps of:

  a. providing at least one environmental sample;

  b. isolating a plurality of genomic DNAs from said environmental sample(s);

  c. determining the abundance of the indicator identified in the method of claim 60 in the plurality of genomic DNAs isolated in step b; and

  d. inferring the abundance of the environmental parameter in said sample(s) based upon the abundance of said indicator in said sample(s).

Claim 66 (Previously submitted). The method according to claim 65, wherein the environmental parameter is subsurface oil or natural gas.

Claim 67 (Previously submitted). The method of claim 65, wherein the abundance of said indicator in said plurality of genomic DNAs is determined using PCR.

Claim 68 (Previously submitted). The method of claim 65, wherein the abundance of said indicator in said plurality of genomic DNAs is determined using a hybridization assay.

Claim 69 (Withdrawn). The method of any one of claims 45, 60 or 65, wherein said environmental sample is selected from the group consisting of a body tissue sample, a body fluid sample, a cell culture and a tissue culture, and said environmental parameter is selected from the group consisting of a medical condition, an acute disease state, a chronic disease state, and a physiological state.